

50449 sequence listing

SEQUENCE LISTING

<110> ZENECA LIMITED

<120> GST SEQUENCES FROM SOYBEAN AND THEIR USE IN THE
PRODUCTION OF HERBICIDE RESISTANT PLANTS

<130> ZENECA CASE PPD50449/WO

<140>

<141>

<150> GB9922346.3

<151> 1999-09-21

<160> 43

<170> PatentIn Ver. 2.0

<210> 1

<211> 499

<212> PRT

<213> Glycine max

<400> 1

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35 40 45Trp Ser Thr Leu Asn Cys Leu Leu Val Gly Asp Lys Ser Val Gln Arg
50 55 60Ser Gly Arg Val Pro Gly Val Gly Leu Val His Leu Pro Leu Ser Leu
65 70 75 80Leu Pro Gly Pro Phe Pro Glu Ser His Trp Lys Gln Gly Cys Glu Leu
85 90 95Ala Pro Ile Phe Asn Glu Leu Val Asp Arg Val Ser Leu Asp Gly Lys
100 105 110Phe Leu Gln Glu Ser Leu Ser Arg Thr Lys Asn Ala Asp Glu Phe Thr
115 120 125Ser Arg Leu Leu Asp Ile His Ser Lys Met Leu Gln Ile Asn Lys Lys
130 135 140Glu Asp Ile Arg Met Gly Ile Val Arg Ser Asp Tyr Met Ile Asp Glu
145 150 155 160Lys Thr Lys Ser Leu Leu Gln Ile Glu Met Asn Thr Ile Ser Thr Ser
165 170 175Phe Ala Leu Ile Gly Cys Leu Met Thr Gly Leu His Lys Ser Leu Leu
180 185 190Ser Gln Tyr Gly Lys Phe Leu Gly Leu Asn Ser Asn Arg Val Pro Ala
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195
200
205
Asn Asn Ala Val Asp Gln Ser Ala Glu Ala Leu Ala Lys Ala Trp Ser
210 215 220
Glu Tyr Asn Asn Pro Arg Ala Ala Ile Leu Val Val Val Gln Val Glu
225 230 235 240
Glu Arg Asn Met Tyr Glu Gln His Tyr Ile Ser Ala Leu Leu Arg Glu
245 250 255
Lys His His Ile Arg Ser Ile Arg Lys Thr Leu Thr Glu Ile Asp Gln
260 265 270
Glu Gly Lys Ile Leu Pro Asp Gly Thr Leu Ser Val Asp Gly Gln Ala
275 280 285
Ile Ser Val Val Tyr Phe Arg Ala Gly Tyr Thr Pro Lys Asp Tyr Pro
290 295 300
Ser Glu Ser Glu Trp Arg Ala Arg Leu Leu Met Glu Gln Ser Ser Ala
305 310 315 320
Ile Lys Cys Pro Thr Ile Ser Tyr His Leu Val Gly Thr Lys Lys Ile
325 330 335
Gln Gln Glu Leu Ala Lys Pro Gly Val Leu Glu Arg Phe Val Glu Asn
340 345 350
Lys Asp His Ile Ala Lys Leu Arg Ala Cys Phe Ala Gly Leu Trp Ser
355 360 365
Leu Glu Asp Ser Asp Ile Val Lys Lys Ala Ile Glu Asn Pro Glu Leu
370 375 380
Phe Val Met Lys Pro Gln Arg Glu Gly Gly Gly Asn Asn Ile Tyr Gly
385 390 395 400
Asp Glu Leu Arg Glu Thr Leu Leu Lys Leu Gln Glu Ala Gly Ser Gln
405 410 415
Glu Asp Ala Ala Tyr Ile Leu Met Gln Arg Ile Phe Pro Ala Thr Ser
420 425 430
Pro Ala Ile Leu Val Arg Asp Gly Asn Trp Asp Thr Gly His Val Ile
435 440 445
Ser Glu Ala Gly Ile Phe Gly Thr Tyr Leu Arg Asn Lys Asp Lys Ile
450 455 460
Ile Ile Asn Asn Glu Ser Gly Tyr Met Val Arg Thr Lys Ile Ser Ser
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Tyr Leu Thr

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<210> 2
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Protein
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<210> 3

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<213> Artificial Sequence

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Protein
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<213> Artificial Sequence

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<210> 6

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<212> DNA

<213> Glycine max

<400> 6

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<210> 7
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 <212> PRT
 <213> Glycine max

<400> 7

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Tyr Lys Tyr Leu Glu Asp Asp Leu Asn Asn Lys Ser Asp Leu Leu Leu
          35          40          45
Lys Tyr Asn Pro Val Tyr Lys Met Ile Pro Val Leu Val His Asn Glu
          50          55          60
Lys Pro Ile Ser Glu Ser Leu Val Ile Val Glu Tyr Ile Asp Asp Thr
          65          70          75          80
Trp Lys Asn Asn Pro Ile Leu Pro Ser Asp Pro Tyr Gln Arg Ala Leu
          85          90          95
Ala Arg Phe Trp Ala Lys Phe Ile Asp Asp Lys Cys Val Val Pro Ala
          100          105          110
Trp Lys Ser Ala Phe Met Thr Asp Glu Lys Glu Lys Glu Lys Ala Lys
          115          120          125
Glu Glu Leu Phe Glu Ala Leu Ser Phe Leu Glu Asn Glu Leu Lys Gly
          130          135          140
Lys Phe Phe Gly Gly Glu Glu Phe Gly Phe Val Asp Ile Ala Ala Val
          145          150          155          160
Leu Ile Pro Ile Ile Gln Glu Ile Ala Gly Leu Gln Leu Phe Thr Ser
          165          170          175
Glu Lys Phe Pro Lys Leu Ser Lys Trp Ser Gln Asp Phe His Asn His
          180          185          190
Pro Val Val Asn Glu Val Met Pro Pro Lys Asp Gln Leu Phe Ala Tyr
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          210          215          220
    
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<210> 8
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 <212> PRT
 <213> Glycine max

<400> 8

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          20          25          30
    
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Glu Tyr Val Glu Glu Asp Leu Arg Asn Lys Ser Asp Leu Leu Leu Lys
35 40 45
Tyr Asn Pro Val His Lys Lys Val Pro Val Leu Val His Asn Gly Lys
50 55 60
Ala Ile Ala Glu Ser Met Val Ile Leu Glu Tyr Ile Asp Glu Thr Trp
65 70 75 80
Lys Asp Gly Pro Lys Leu Leu Pro Ser Asp Ser Tyr Lys Arg Ala Gln
85 90 95
Ala Arg Phe Trp Cys His Phe Ile Gln Asp Gln Leu Met Glu Ser Thr
100 105 110
Phe Leu Val Val Lys Thr Asp Gly Glu Ala Gln Gln Lys Ala Ile Asp
115 120 125
His Val Tyr Glu Lys Leu Lys Val Leu Glu Asp Gly Met Lys Thr Tyr
130 135 140
Leu Gly Glu Gly Asn Ala Ile Ile Ser Gly Val Glu Asn Asn Phe Gly
145 150 155 160
Ile Leu Asp Ile Val Phe Cys Ala Leu Tyr Gly Ala Tyr Lys Ala His
165 170 175
Glu Glu Val Ile Gly Leu Lys Phe Ile Val Pro Glu Lys Phe Pro Val
180 185 190
Leu Phe Ser Trp Leu Met Ala Ile Ala Glu Val Glu Ala Val Lys Ile
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Leu Ser Ala Leu Lys Ser Ser Ser Ala Thr Glu
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<210> 9
<211> 223
<212> PRT
<213> Glycine max

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35 40 45
Val Tyr Lys Lys Thr Pro Val Leu Val His Asn Gly Lys Pro Leu Cys
50 55 60
Glu Ser Met Leu Ile Val Glu Tyr Ile Asp Glu Ile Trp Ala His Asn
65 70 75 80
Ser Leu Leu Pro Ala Asp Pro Tyr Glu Arg Ala Leu Ala Arg Phe Trp

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85

90

95

Val Lys Tyr Ala Asp Asp Asp Met Phe Ser Ala Val Ile Ala Phe Phe
 100 105 110
 Leu Ser Asn Asn Asp Glu Glu Arg Glu Lys Ser Ile Glu Lys Ile Trp
 115 120 125
 Glu His Leu Arg Val Val Glu Asn Gln Cys Phe Gly Asp Gln Lys Lys
 130 135 140
 Phe Phe Gly Gly Asp Ile Ile Asn Ile Met Asp Ile Ala Phe Gly Ser
 145 150 155 160
 Ile Phe Lys Ile Leu Val Val Ala Glu Asp Ile Leu Asp Ala Lys Val
 165 170 175
 Leu Glu Asp Glu Lys Phe Pro His Leu His Ser Trp Tyr Asn Asn Phe
 180 185 190
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 210 215 220

<210> 10

<211> 232

<212> PRT

<213> Glycine max

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 Val Val Glu Glu Thr Leu Asn Pro Lys Ser Glu Leu Leu Lys Ser
 35 40 45
 Asn Pro Val His Lys Lys Ile Pro Val Phe Phe His Gly Asp Lys Val
 50 55 60
 Ile Cys Glu Ser Ala Ile Ile Val Glu Tyr Ile Asp Glu Val Trp Ser
 65 70 75 80
 Asn Asn Ala Leu Ser Ile Leu Pro Gln Asn Ala Tyr Asp Arg Ala Asn
 85 90 95
 Ala Arg Phe Trp Val Ser Tyr Ile Asp Asp Lys Trp Leu Thr Ser Leu
 100 105 110
 Lys Ser Val Leu Ala Thr Glu Asp Asp Glu Ala Lys Lys Leu His Phe
 115 120 125
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 130 135 140
 Cys Ser Glu Gly Lys Ala Tyr Phe Gly Gly Asp Thr Ile Gly Phe Val
 145 150 155 160

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Asp Ile Gly Phe Gly Ser Phe Leu Ser Phe Ile Arg Val Ser Glu Asn
165 170 175
Met Asn Glu Arg Lys Leu Leu Asp Glu Thr Lys Tyr Pro Gly Leu Thr
180 185 190
Leu Trp Ala Glu Thr Phe Ala Ala Asp Pro Ala Val Lys Gly Leu Leu
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Trp Ala Ala Ala Ala Ala Ala Lys
225 230

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<211> 885
<212> DNA
<213> Glycine max

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atgaaagcta cttgtctatg tttcgttatt gcggttgat tttcattttt caatgaatta 780
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<211> 899
<212> DNA
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<400> 12

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<210> 13

<211> 840

<212> DNA

<213> Glycine max

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gaatcgtttt gttatgcgtg ttcttttagt ttccactcca ttattaggat gtcttgacat 780
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<210> 15
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 <223> Description of Artificial Sequence:PRIMER

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<210> 16
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<210> 17
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 <400> 18
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 <210> 19
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 <210> 21
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 <213> Artificial Sequence

 <220>
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<210> 22
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 <223> Description of Artificial Sequence:PRIMER

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 <210> 23
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 <223> Description of Artificial Sequence:PRIMER

 <400> 23
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 <210> 24
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 nucleic acid sequence P32110

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 aaaaaataaa aattgttaac attataaaaat taaaaaacia atttatgaaa aaaaagggtta 360
 acaaatataa aacaaactac aaatagtaaa ataacgtttt taaaaaaaaa aggagggttac 420
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 ggtccaaatt cattgatgat aaggtaactc aacatttcaa aaatcttctt agttttcatg 1620
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50449 sequence listing

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 tatataataa taattattgc aagttggaag tcgtgtaagc atgtttcatg actatatgag 2700
 ttaacaatat actgtcttgc ctctgcaacc ttcattggatt ctaaaattat tcccttggtc 2760
 gca 2763

<210> 26

<211> 1137

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Mungbean
 Sequence U20809

<400> 26

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 aagggtccag tgtttgttca tggtgacaaa ccccttccag agtcccttgt gattgttgag 240
 tacatcgatg agacatggaa caacaacccc atcttggtct ctgatcctta ccagagagcc 300
 ttggctcggt tctgggtcaa attcatcgat gacaagattg tgggtgcttc gtggaaatct 360
 gttttcacag ttgatgagaa agagcgtgag aagaatattg cagaaacata tgagagtctg 420
 cagtttcttg agaatgagat aaaggagaag aagttctttg gaggagaaga gcttgggttg 480
 gtagatattg ctgctgtcta tgtagcattt tggatccctt tgattcaaga aatagcagga 540
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 caccaaaaag tgagtatttc cttacagaag ctttttaaat attaagtagt taattccata 1020
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50449 sequence listing

<210> 27
 <211> 2038
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Tobacco
 sequence Q03663

<400> 27

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gtcaagtcgt gattgggata agaaaataga aatttattta tactccagat caagccgtga 180
ttggaatgag ataatagaaa agtatgatag tacatgagta acatcaagtt ggaaattaag 240
ggaaggaaat tagagaaaga actgaagaat atccaaatat tctttacgtc caaatttgat 300
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gaaagaagaa gacacaaact gtgtttggta ttattatagt tttttctttt agagaattga 420
ttgtacatat aagaaatata atataagatt tagaaataag attattagaa aaatcaaaca 480
tcaaagtatt tattttaaat tctttttcca atggacattc ccattctgaa aaaaaagaga 540
tataaatatg gaagtaaaaa ttaatcagat cgtaaagtgt agaaaatatt aattaacaca 600
ttaaccataa ccagtctact ttatttaaca aaaagcacat ctgaratarc aaaaaagtgt 660
ttaacttcat gcattgacaa tttaaaatta ttttgcaaca tcgggtaaaa ctattttaca 720
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tgttgtctct tgcaactatg atcctccagg taattataga ggcgaaagtc catactaatt 1440
gaaacgacct acgtccattt cacgttaata tgtatggatt gttctgcttg atatcaagaa 1500
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50449 sequence listing

gtaatcctct gaagtggatc tataaaaaga ccaagtggc ataattaagg ggaaaaatat 1620
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gaatcatgtg ttgatggctt agctacttgc gatattacga gcaaaattct taactacatg 1740
ccttaggaac aagcttacac agttcatata atctactaga gggccaaaaa catgaaaatt 1800
accaatttag atggtaggag gatattgaaa gtggagcagc tagttttaat aactgaccgt 1860
tagtcttaaa attgacggtg taaaaatatt tacataatca ggatcattat aaggtaatta 1920
taggtaaata tttatgacga attctcaata gtaatctgaa aaaaaattgt aactaaccta 1980
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<210> 28

<211> 2796

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Potato- Derived
nucleic acid sequence P32111

<400> 28

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aaccacaactc aatattagaa aatcaaaaat tttagtgcac tcattttataa aaaaaaaaaa 180
aattacttat gcagttcttg aaccctttgt gagacgagag ggagttgctc ggatggtaag 240
cacccttcac tttcaacccg aagggttgcga gtttgagtca ccaacggagc aaaaagggtg 300
ggagctccta gaaagggtta aaaaaaaaaa aaaaattaat aaaaaaatac cttttatgaa 360
atttctcatt ccgctactgc acttctcccc tgatcttcct cgtgttttca attattaatt 420
ctatattcat gacaccatgt gatgtttctc tgggtagtcc taaaaataga ggtattgaaa 480
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atgttttaat taggtataat acataaatat ttcctttaat tttatctcat tttatattta 720
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gcatgcttag ttttactttc caaattgaaa tttatattag aattgaattc aggaagaatt 840
ttgtagggtc aactaaatta tatatatata tataaaaaaa taaaaattat tagacgcttc 900
gactatttac ttacttttaa atttgaattt tcgtacgaat aaaattattt gtcagagaaa 960
agtcttttag ctattcacat gctaggaagt ttcacttttg gtggatcagt gattgtatat 1020
tatttaatat atatcaattt tctcatcaaa ctgaaaatga aagataaaat taatattaaa 1080

50449 sequence listing

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atttttttaa ttttatacta aaaaacatgt cacatgaata ttgaaatta taaaattatc 1260
aaaaataaaa aaagaatatt tctttaacaa attaaaaatg aaaatatgat aaataaatta 1320
aactattcta tcattgattt ttctagccac cagatttgac caaacagtgg gtgacatgag 1380
cacataagtc atctttattg tattttatta ctactccaa aaatataggg aatatgttta 1440
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tttaatgcat ccttattttt tcctctataa aaaaaagact agacaccaag ggagaccaac 1560
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<210> 29
 <211> 1289
 <212> DNA

50449 sequence listing

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Arabidopsis
P46421

<400> 29

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aacatctgtt tccttctaga ctcttcgcat ttacatcaca ctgccgacca tataaaacgg 180
caaagttcgt cgtcgtttta tcacaagacc atcaacacca taaggctata aatccaagct 240
aaaaggtagt gattaactcc acaaaaccag aaaaactaca tttctaacat atagaagaaa 300
cagagaaaaa gagagagaga cccctaattg ctgagaaaga agaagtgaag cttttgggga 360
tatgggcgag cccttttagc cgtcgggtcg agatggctct caaactcaa ggcataccgt 420
acgagtacgt ggaagagata ctggagaaca aaagcccttt gcttcttgct cttaaccta 480
ttcacaagaa agtccctgtt cttgtccaca atggtaaaac cattctcgag tctcatgtga 540
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aaaattgcat gtcaaataat aaacaattgg ttctgctttg ttaatttatc aaacaagtaa 720
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atatcaatgg caagagcaga cgagaaagga agagaagttt tagccgagca ggtaagagaa 840
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cttgatcatg caatgtttgt atggttatgt tgttgtttat ttattgaat atctttgtat 1200
gttgtgtggt tgagaagtga ggttttatca tcatctctca cgttatctta ttggtccca 1260
gccactatth agaattaatg gtaaagctt 1289
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<210> 30

<211> 1339

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Arabidopsis
Genomic sequence

<400> 30

50449 sequence listing

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agagataaaa aaaaatttga tagggaacgt tataaatatg ttgtaaagtc aacatctgtt 180
tccttctaga ctcttcgcat ttacatcaca ctgccgacca tataaaacgg caaagttcgt 240
cgtcgtttta tcacaagacc atcaacacca taaggctata aatccaagct aaaaggtagt 300
gattaactcc aaaaaaccag aaaaactaca tttctaacat atagaagaaa cagagaaaaa 360
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cccttttagc cgtcgggtcg agatggctct caaactcaaa ggcataccgt acgagtacgt 480
ggaagagata ctggagaaca aaagcccttt gcttcttgct cttaacccta ttcacaagaa 540
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gtcaaataat aaacaattgg ttctgctttg ttaatttatc aaacaagtaa ttttctatta 780
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tggaagtgat tacagaggag aagtttccag agttcaagag atgggttagg aatttggaga 1080
aggttgagat tgtaaagat tgtgttccac caagagagga acatgtagaa cacatgaact 1140
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caatgtttgt atggttatgt tgttgtttat tttattgaat atctttgtat gttgtgtggg 1260
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1339

<210> 31

<211> 968

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Papaya AJ000923

<400> 31

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tggaatgaga atcagaatcg ctttagccga gaagggtatt cactacgagt acaaggaaga 180
gaatctgaga aacaagagtc cttactcct gcagatgaac ccggtacaca agaaaatccc 240

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50449 sequence listing

gggtctcatc cacaatggta aacccatctg tgagtctttg atccagattc agtacataga 300
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<210> 32

<211> 1040

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Spruce AF051214

<400> 32

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 aggttactaa tttagtttta atagaccagg agaagatgcc gctgttaagc acatggatga 660
 atcgattctg tgaggccgat ggagtgaag acgttatgcc ggatccggcc aagttgcagg 720
 aatttatatc cgccatcaga gtcagattta catcaccacc tgctgccaat taggggaagc 780

50449 sequence listing

cattcggcca ttaaattggat gttatcgtcc gcattgtttt tggttttatg ctgtcagttt 840
 gaatgttggt atgctttttg aattgttggt gtttaatggg aataattcta tcgccaatc 900
 tagcaccgtg tgattcgcta tcagttctca ccgtgttcca tgtaacttcg atttcatgat 960
 tttgggagat agaacaaaaa ttcattggaaa tgtgtgttag tgttttatat ttgaaaaggg 1020
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<210> 33

<211> 902

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Wheat AF004358

<400> 33

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<210> 34

<211> 1127

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Spruce AF051238

<400> 34

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50449 sequence listing

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 tgcccgttc tgggctgcct ttgtagacga taagctcgtt ccatgtatgc ggagagtttt 420
 cgctggccat ggcgagcagc tacagaaaga agcggaagat ctggttaca actttcattt 480
 gatagaggaa gctctgcgaa ccaacagctg cttctcagga aaagcgtatt ttggagggga 540
 taagataggc ttgcttgaca tcgcattggg tggtatgttg gcggttctca aaggcctcga 600
 gaaggctacc gataccgtta taatagatcc ggagaagatg ccgttgctga gcgcatggat 660
 ggaccgattt tgtcaatcca atggagtga agaagtaatg cccgatccgg ccaagcagct 720
 ggaatctcta tcagctagga gagccagact tgcacacct gctggcaatt agggcaagcc 780
 atgtcggcct tataaactga ggatagacag atggattata aacttattat tcgtagtact 840
 tgtcctttta ttcattgttg cagcttcagc gttttaattc ttgctgtttt atgtgaataa 900
 gtctgaataa tgtttgggtg aatctcgcct gtactatagc tggcattcac ctgtttattg 960
 tacgctgatt tagtttgaac aagttttggt gaatctcccc tgtactgaag ctggcattcc 1020
 cctgttcaat gtgcgctgat ttagtttgaa taagtttttg atgaatctcg cttgtactgt 1080
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<210> 35

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 35

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<210> 36

<211> 234

<212> PRT

<213> Glycine max

<400> 36

Met Ser Lys Ser Glu Asp Leu Lys Leu Leu Gly Gly Trp Phe Ser Pro
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Phe Ala Leu Arg Val Gln Ile Ala Leu Asn Leu Lys Gly Leu Glu Tyr
 20 25 30

Glu val val Glu Glu Thr Leu Asn Pro Lys Ser Asp Leu Leu Leu Lys

50449 sequence listing

35
 Ser Asn Pro Val His Lys Lys Ile Pro Val Phe Phe His Gly Asp Lys
 50 55 60
 Val Ile Cys Glu Ser Ala Ile Ile Val Glu Tyr Ile Asp Glu Ala Trp
 65 70 75 80
 Thr Asn Val Pro Ser Ile Leu Pro Gln Asn Ala Tyr Asp Arg Ala Asn
 85 90 95
 Ala Arg Phe Trp Phe Ala Tyr Ile Asp Glu Lys Trp Phe Thr Ser Leu
 100 105 110
 Arg Ser Val Leu Val Ala Glu Asp Asp Glu Ala Lys Lys Pro His Phe
 115 120 125
 Glu Gln Ala Glu Glu Gly Leu Glu Arg Leu Glu Glu Val Phe Asn Lys
 130 135 140
 Tyr Ser Glu Gly Lys Ala Tyr Phe Gly Gly Asp Ser Ile Gly Phe Ile
 145 150 155 160
 Asp Ile Gly Phe Gly Ser Phe Leu Ser Trp Met Arg Val Ile Glu Glu
 165 170 175
 Met Ser Gly Arg Lys Leu Leu Asp Glu Lys Lys His Pro Gly Leu Thr
 180 185 190
 Gln Trp Ala Glu Thr Phe Ala Ala Asp Pro Ala Val Lys Gly Ile Leu
 195 200 205
 Pro Glu Thr Asp Lys Leu Val Glu Phe Ala Lys Ile Leu Gln Leu Lys
 210 215 220
 Trp Thr Ala Ala Ala Ala Ala Ala Ala Lys
 225 230

<210> 37
 <211> 222
 <212> PRT
 <213> Glycine max

<400> 37

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 1 5 10 15
 Pro Phe Leu His Arg Val Gln Ile Ala Leu Lys Leu Lys Gly Val Glu
 20 25 30
 Tyr Lys Tyr Leu Glu Asp Asp Leu Asn Asn Lys Ser Asp Leu Leu Leu
 35 40 45
 Lys Tyr Asn Pro Val Tyr Lys Met Ile Pro Val Leu Val His Asn Glu
 50 55 60
 Lys Pro Ile Ser Glu Ser Leu Val Ile Val Glu Tyr Ile Asp Asp Thr
 65 70 75 80
 Trp Lys Asn Asn Pro Ile Leu Pro Ser Asp Pro Tyr Gln Arg Ala Leu
 85 90 95

50449 sequence listing

Ala Arg Phe Trp Ala Lys Phe Ile Asp Asp Lys Cys Val Val Pro Ala
100 105 110
Trp Lys Ser Ala Phe Met Thr Asp Glu Lys Glu Lys Glu Lys Ala Lys
115 120 125
Glu Glu Leu Phe Glu Ala Leu Ser Phe Leu Glu Asn Glu Leu Lys Gly
130 135 140
Lys Phe Phe Gly Gly Glu Glu Phe Gly Phe Val Asp Ile Ala Ala Val
145 150 155 160
Leu Ile Pro Ile Ile Gln Glu Ile Ala Gly Leu Gln Leu Phe Thr Ser
165 170 175
Glu Lys Phe Pro Lys Leu Ser Lys Trp Ser Gln Asp Phe His Asn His
180 185 190
Pro Val Val Asn Glu Val Met Pro Pro Lys Asp Gln Leu Phe Ala Tyr
195 200 205
Phe Lys Ala Arg Ala Gln Ser Phe Val Ala Lys Arg Lys Asn
210 215 220

<210> 38
<211> 895
<212> DNA
<213> Glycine max

<400> 38

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gtctagaata tgaggttggt gaagagacct tgaatcccaa aagtgacctg cttcttaagt 180
ccaaccctgt gcacaagaaa atcccagttt tcttccatgg agataaagtc atttgtgaat 240
ctgcaatcat agttgagtac attgatgagg cttggactaa tgttccctcc atccttcac 300
aaaatgctta tgatcgtgct aatgctcgat tttggtttgc ctacattgat gagaagtggg 360
ttacgtcctt gagaagtgtt ctagtggctg aagatgatga ggcaaagaag ccacactttg 420
agcaagcaga agaagggcct gagagggttg aagaagtgtt caacaagtac agtgaaggga 480
aggcctattt cggaggagat agcattggat tcattgacat tggttttggg agcttcttga 540
gttggtgatgag agtcatagag gagatgagtg gaagaaaatt gcttgatgaa aagaagcacc 600
ctggtttgac ccaatgggct gaaacgtttg ctgctgatcc tgctgtgaag ggcattcttc 660
cagagactga taagcttggt gagtttgcca agattcttca gctaaaatgg actgctgcag 720
cagctgcagc tgcaaagtaa atggaatcaa attaattgcg agagtatttt caaaattgtt 780
gtccaagtgtg tttttatctc aggctatgtt gttgcaactt tatttattta aaagttattt 840
taaatttaaa atgtaaaata ttaagaaagt ttaagtaagt tagttgaaaa atttt 895

50449 sequence listing

<210> 39
 <211> 895
 <212> DNA
 <213> Glycine max

<400> 39

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agattgctct caagttgaag ggagttgaat acaaatatatt ggaagacgat ttgaacaaca 180
agagtgattt gtcctcaag tataaccag tttacaaaat gattccagtg cttgttcaca 240
atgagaagcc catttcagag tcccttgtaga ttgttgagta cattgatgac acatggaaaa 300
acaatcccat cttgccttct gatccctacc aaagagcctt ggctcgtttc tgggctaagt 360
tcattgatga caagtgtgtg gttccagcat ggaaatctgc ttttatgact gatgagaaag 420
agaaagagaa ggctaaagaa gagttatttg aggctctgag ttttcttgag aatgagttga 480
agggcaagtt ttttggtgga gaggagtttg gctttgtgga tattgctgct gtgtaatac 540
ctataattca agagatagca gggttgcaat tggtcacaag tgagaaattc ccaaagctct 600
ctaaatggag ccaagacttt cacaaccatc cagttgtcaa cgaagttagt cctcctaagg 660
atcaactttt tgcctatttc aaggctcggg ctcaaagctt cgttgctaaa agaaagaatt 720
aatatagtga gactcagaat ttccatcgag gtttcagtat tgtatgaaat gaaagctact 780
tgtctatgtt tcgttattgc gggtgtattt tcatttttca atgaattatg tgatatagga 840
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<210> 40
 <211> 977
 <212> DNA
 <213> Glycine max

<400> 40

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gaagcttttg ggagctactg gaagcccatt tgtgtgcagg gttcagattg ccctcaagtt 180
gaagggagtt caatacaaat ttttggaga aaatttgagg aacaagagtg aactgcttct 240
caaatccaac ccagttcaca agaaggttcc agtgtttatt cacaatgaga agcccatagc 300
agagtctctt gtgattgttg aatacattga tgagacatgg aagaacaacc ccatcttgcc 360
ttctgatcct taccaaagag ctttggtcgt tttctggtcc aaattcattg atgacaaggt 420
tgtgggtgct gcatggaaat atatttatac tgttgatgag aaagagcgtg agaagaatgt 480
tgaagagtca tatgaggctc tgcagtttct tgagaatgag ctgaaggaca agaagttttt 540
tggaggagag gaaattgggt tggtagatat tgctgctgtc ttcatagcac tttggatccc 600
  
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50449 sequence listing

tataattcaa gaagtattgg gtttgaagtt attcacaagt gagaaatttc ctaagctcta 660
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 tcaacttttt gccttctaca aagcctgccca tgaaagtctt tctgcttcaa aatagactta 780
 ttttaaggata gtttgttgaa ctactggctc ctcatttggt agttattgca gtttgaattt 840
 catgtcaatt tgggtttata tgtaatttag taacctggga tatctcccat ggagaaaata 900
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 aaaaaaaaaa aaaaaaa 977

<210> 41
 <211> 1006
 <212> DNA
 <213> Glycine max

<400> 41

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 aagaaaattt gaggaacaag agtgaactgc ttctcaaadc caaccagtt cacaagaagg 180
 ttccagtgtt tattcacaat gagaagccca tagcagagtc tcttgtgatt gttgaatata 240
 ttgatgagac atggaagaac aaccccatct tgccttctga tccttaccaa agagccttgg 300
 ctcgtttctg gtccaaattc attgatgata aggtttttgg tgctgcatgg aaatccgttt 360
 tcacagctga tgagaaagag cgtgagaaga atgttgagga agcaattgag ctctgcagtt 420
 tcttgagaat gagataaagg acaagaagtt ctttggagga gaggagattg ggttggtaga 480
 tattgtctgt gtctacatag cattttgggt ccctatgggt caagaaattg cagggttgga 540
 gttattcaca agtgagaaat ttcctaagct ccacaattgg agccaagaat ttttgaacca 600
 tccaattgtc aaagaaagtc tgccccctag agatcctgtt ttctcctttt tcaaggggtc 660
 ctatgaaagc ctttttggtt caaaatagat ttgatgatgt ggtgtgagac ttagtatttc 720
 taagaattat gtgtttgtta aaggcttcta tgaaagcctc actgcttcaa aatagattca 780
 tgtatgtgag actcagaatc tctggggaaa atttgtgtgt gtgtggacta cttgttttgt 840
 ttgtcattga gctatatcgc tgtaatttag gattttgttt caaaatgatg cttataagtt 900
 gtaatctagg atttctccct ttgaaatcct aggttgttct tgacatttgc tatttcaaag 960
 aataaatata tagcatcttt ctatttctca aaaaaaaaaa aaaaaa 1006

<210> 42
 <211> 885
 <212> DNA
 <213> Glycine max

<400> 42

50449 sequence listing

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ccaagaggggt ggaattggcc ctttaatttta agggcatacc ctatgagtat gttgaagaag 120
acttgagaaa taagagtgat ttgcttctaa agtacaaccc tgttcacaag aagggttcctg 180
tacttgttca taatggaaag gccattgctg aatccatggg gatccttgag tatattgatg 240
aaacatggaa agatgggtcct aaactgcttc caagtgattc ttacaaacga gcccaagctc 300
gattctgggtg tcatttcacg caggatcagt taatggagag cacttttcta gtagtcaaaa 360
ctgatggaga agcacaacaa aaggccattg accacgtgta tgagaaactg aaagtgctag 420
aagatggaat gaagacctat ctggggagaag gcaatgctat tatctctggg gttgaaaaca 480
actttggaat ccttgacatt gtgttttggg ctttatatgg tgcctacaag gctcatgaag 540
aagttattgg cctcaagttc atagtgccag aaaagtttcc tgtgttgggt tcttggttga 600
tggctattgc tgagggttga gctgtgaaaa ttgcaactcc tccacatgaa aaaacagtgg 660
gaattcttca gttgttcagg ctgtctgcac tgaaatcttc ttctgccaca gaatgatata 720
tacttcaaca ctttaataga ctgtccatcg tttgcttctt ctgagagtct ttagtgtatg 780
tatctttcaa taacaggatg agtaacacct gagtatgtaa agcgtgatga tatagagata 840
tacctctata tatcaaatac tcttctataa aaaaaaaaaa aaaaa 885

<210> 43

<211> 991

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SSM.PK0067.G5

<400> 43

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aagaagaagt gaggtctattg ggcaagtggg ccagcccatt tagcaacaga gtagaccttg 180
ctctcaagct caaggggtgtt ccctacaaat actccgagga agatcttgct aacaagagtg 240
ctgatcttct caagtacaac cccgttcaca agaagggttcc ggttttgggt cacaatggga 300
accattggcc cgagtcactc atcattgttg aatacataga tgagacgtgg aaaaataacc 360
cactattgcc tcaagacca tatgaaagag ccttggctcg tttttgggtc aagaccttag 420
atgacaagat cttgccagct atatggaatg cttgctggag tgacgagaat gggcgtgaga 480
aagcagtgga ggaagccttg gaagcattga aaatcctaca ggaaacactg aaagacaaga 540
aattcttttg aggagagagc ataggattgg tagatattgc tgccaatttc attgggtatt 600
gggttgccat attgcaagag attgcagggg tggagttgct caccattgag aaatttccca 660
agttatataa ttggagtcaa gactttatca accaccctgt gatcaaggag ggtctgcctc 720

50449 sequence listing

ctagagatga attgtttgct ttcttcaaag cttctgctaa aaagtagaac catttttagag 780
gtaggattca taataagtta gtatgatttt gttgggaaac aattatcttg ttgtgagcaa 840
aggattgttc tgttttaaata ttaattgact gtgatttggt tgggtattgg ctattttaat 900
ttaaactaaa aaaagtgttc agttttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 991